

Blast 2 Sequence:

Exhibit 4

[NCBI](#)[E. strez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site [Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  ☒ Matrix  ☒

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch: ☐ Use Mega BLAST Strand option  ☒Open gap  and extension gap  penaltiesgap x\_dropoff  expect  word size  Filter ☒ Sequence 1 Enter accession or GI  or download from fileor sequence in FASTA format from:  to: Sequence 2 Enter accession or GI  or download from fileor sequence in FASTA format from:  to: 

accggaagcgctcagacttggtcg

  Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

4/28/2002

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]**Match:  Mismatch:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☒

<b>Sequence</b>	gi	Homo sapiens endothelial differentiation, sphingolipid G-protein-	<b>Length</b> 2753
<b>1</b>	13027635	coupled receptor, 1 (EDG1), mRNA	

<b>Sequence</b>	lcl seq_2	<b>Length</b> 25
<b>2</b>		

No significant similarity was found